

Appendix I: Alignment of NP_003204 with AAC50763 (SEQ ID NO: 7)

BLASTP 2.2.23+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: Z8246KTB01S

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

11,049,075 sequences; 3,763,785,421 total letters

Query= gi|4507427|ref|NP_003204.1| TEA domain family member 4 [Homo sapiens]
Length=434

ALIGNMENTS

>gb|AAC50763.1| transcription factor RTEF-1 [Homo sapiens]
Length=434

Score = 907 bits (2345), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/434 (100%), Positives = 434/434 (100%), Gaps = 0/434 (0%)

Query 1	MEGTAGTITSNEWSSPSTSPEGSTASGGSQALDKPIDNDGEGVWSPDIEQSFQEALAIYPP	60
Sbjct 1	MEGTAGTITSNEWSSPSTSPEGSTASGGSQALDKPIDNDGEGVWSPDIEQSFQEALAIYPP	60
Query 61	CGRRKIIILSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHIQLARRKAREIQAKLKDQ	120
Sbjct 61	CGRRKIIILSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHIQLARRKAREIQAKLKDQ	120
Query 121	AAKDKALQSMAAMSSAQIIISATAFHSSMRLARGPGRPAVSGFWQGALPGQAETSHDVKPF	180
Sbjct 121	AAKDKALQSMAAMSSAQIIISATAFHSSMRLARGPGRPAVSGFWQGALPGQAETSHDVKPF	180
Query 181	SQQTYAVQPPLPLPGFESPAGPAPSPSAPPAPPWQGRRRGSSKLWMLEFSAFLEQQQDPD	240
Sbjct 181	SQQTYAVQPPLPLPGFESPAGPAPSPSAPPAPPWQGRRRGSSKLWMLEFSAFLEQQQDPD	240
Query 241	TYNKHLFVHIGQSSPSYLRPYLEAVDIRQIYDKFPEKKGGLKDLFERGPSNAFFLVKFWA	300
Sbjct 241	TYNKHLFVHIGQSSPSYLRPYLEAVDIRQIYDKFPEKKGGLKDLFERGPSNAFFLVKFWA	300
Query 301	DLNTNIEDEGSSFYGVSSQYESPENMIITCSTKVCSTFGKQVVEKVEYARYENGHYSYR	360
Sbjct 301	DLNTNIEDEGSSFYGVSSQYESPENMIITCSTKVCSTFGKQVVEKVEYARYENGHYSYR	360
Query 361	IHRSPLECEYMINFIHLKHLPEKYMMSVLENFTILQVVTNRDTQETLLCIAYVFEVSAS	420

Sbjct	361	IHRSP L CEYMINFIHKLKHLPEKYMMNSVLENFTILQVVTNRDTQETLLCIAYVFEVSAS	420
Query	421	EHGAQHHIYRLVKE	434
		EHGAQHHIYRLVKE	
Sbjct	421	EHGAQHHIYRLVKE	434